

AMENDMENTS TO THE CLAIMS

Claims 1-33: (Canceled).

34. (Currently Amended) ~~A microorganism~~ An isolated microorganism belonging to enterobacteria selected from the group consisting of the genus *Enterobacter*, *Pantoea*, *Klebsiella*, *Erwinia* and *Serratia* and having L-glutamic acid productivity which is transformed by a polynucleotide sequence encoding a citrate synthase obtained from *Corynebacterium glutamicum* or *Brevibacterium lactofermentum*,

wherein the transformed microorganism has enhanced L-glutamic acid productivity as compared to the untransformed microorganism.

35. (Previously Presented) The microorganism of claim 34, which is transformed by a polynucleotide sequence encoding a citrate synthase obtained from *Corynebacterium glutamicum*.

36. (Previously Presented) The microorganism of claim 34, which is transformed by a polynucleotide sequence encoding a citrate synthase obtained from *Brevibacterium lactofermentum*.

37. (Previously Presented) The microorganism of claim 34, wherein the microorganism belonging to enterobacteria is a bacterium belonging to the genus *Enterobacter*.

38. (Previously Presented) The microorganism of claim 37, wherein the microorganism is *Enterobacter agglomerans*.

39. (Previously Presented) The microorganism of claim 34, wherein the microorganism belonging to enterobacteria is a bacterium belonging to the genus *Klebsiella*.

40. (Previously Presented) The microorganism of claim 39, wherein the microorganism is *Klebsiella planticola*.

41. (Previously Presented) The microorganism of claim 34, wherein the polynucleotide is obtained from *Corynebacterium glutamicum* or *Brevibacterium lactofermentum* chromosomal DNA by the polymerase chain reaction using oligonucleotide primers of SEQ ID NO: 1 and SEQ ID NO: 2.

42. (Previously Presented) The microorganism of claim 34, wherein the microorganism belongs the genus *Pantoea*.

43. (Previously Presented) The microorganism of claim 34, wherein the microorganism belongs the genus *Klebsiella*.

44. (Previously Presented) The microorganism of claim 34, wherein the microorganism belongs the genus *Erwinia*.

45. (Previously Presented) The microorganism of claim 34, wherein the microorganism belongs the genus *Serratia*.

46. (Previously Presented) A process for producing L-glutamic acid, comprising:

culturing the microorganism of claim 34 in a liquid medium to produce and accumulate L-glutamic acid in the medium and collecting the L-glutamic acid from the medium.

47. (Previously Presented) The process of Claim 46, wherein the enterobacteria is of the genus *Enterobacter* or *Klebsiella*.

48. (Previously Presented) The process of Claim 46, wherein the enterobacteria is *Enterobacter agglomerans* or *Klebsiella planticola*.

49. (Previously Presented) A process for producing L-glutamic acid, comprising:  
isolating a polynucleotide sequence encoding a citrate synthase obtained from a coryneform bacterium, wherein the polynucleotide is obtainable by the polymerase chain reaction using oligonucleotide primers of SEQ ID NO: 1 and SEQ ID NO: 2;  
transforming an enterobacteria with said isolated polynucleotide;  
culturing said enterobacteria in a liquid medium to produce and accumulate the L-glutamic acid, wherein the transformed enterobacteria has enhanced L-glutamic acid productivity as compared to the untransformed enterobacteria; and  
collecting the L-glutamic acid produced.

50. (Previously Presented) The process of Claim 49, wherein the bacterium is *Corynebacterium glutamicum* or *Brevibacterium lactofermentum*.

51. (Previously Presented) The process of Claim 49, wherein the enterobacteria is of the genus *Enterobacter* or *Klebsiella*.

52. (Previously Presented) The process of Claim 49, wherein the enterobacteria is *Enterobacter agglomerans* or *Klebsiella planticola*.

SUPPORT FOR THE AMENDMENTS

Claims 1-33 were previously canceled.

Claim 34 has been amended.

The amendment of Claim 34 is supported by the specification at pages 4-32 and the original claims.

No new matter is believed to have been added to the present application by the amendments submitted above.